

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Administrators of Tulane Educational Fund  
Philipp, Mario T.
- (ii) TITLE OF INVENTION: Surface Antigens and Proteins Useful in Compositions for the Diagnosis and Prevention of Lyme Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Howson and Howson
  - (B) STREET: Spring House Corporate Cntr., P.O. Box 457
  - (C) CITY: Spring House
  - (D) STATE: Pennsylvania
  - (E) COUNTRY: USA
  - (F) ZIP: 19477
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 60/051,271
  - (B) FILING DATE: 30-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Bak, Mary E.
  - (B) REGISTRATION NUMBER: 31,215
  - (C) REFERENCE/DOCKET NUMBER: TUL2APCT
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 215-540-9200
  - (B) TELEFAX: 215-540-5818

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1047 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1047

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAG AAT AAT GAT CAT GAT AAT CAT AAG GGG ACT GTT AAG AAT GCT GTT Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Val Lys Asn Ala Val	48
1 5 10 15	
GAT ATG GCA AAG GCC GCT GAG GAA GCT GCA AGT GCT GCA AGT GCT GCT Asp Met Ala Lys Ala Ala Glu Glu Ala Ala Ser Ala Ala Ser Ala Ala	96
20 25 30	
ACT GGT AAT GCA GCG ATT GGG GAT GTT GTT AAG AAT AGT GGG GCA GCA Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala	144
35 40 45	
GCA AAA GGT GGT GAG GCG GCG AGT GTT AAT GGG ATT GCT AAG GGG ATA Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile	192
50 55 60	
AAG GGG ATT GTT GAT GCT GCT GGA AAG GCT GAT GCG AAG GAA GGG AAG Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys	240
65 70 75 80	
TTG GAT GCT ACT GGT GCT GAG GGT ACG ACT AAC GTG AAT GCT GGG AAG Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys	288
85 90 95	
TTG TTT GTG AAG AGG GCG GCT GAT GAT GGT GAT GCA GAT GAT GCT Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Asp Ala	336
100 105 110	
GGG AAG GCT GCT GCG GTT GCT GCA AGT GCT GCT ACT GGT AAT GCA Gly Lys Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala	384
115 120 125	
GCG ATT GGA GAT GTT AAT GGT GAT GTG GCA AAA GCA AAA GGT GGT Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Gly Gly	432
130 135 140	
GAT GCG GCG AGT GTT AAT GGG ATT GCT AAG GGT ATA AAG GGG ATT GTT Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val	480
145 150 155 160	
GAT GCT GCT GAG AAG GCT GAT GCG AAG GAA GGG AAG TTG AAT GCT GCT Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala	528
165 170 175	
GGT GCT GAG GGT ACG ACT AAC GCG GAT GCT GGG AAG TTG TTT GTG AAG Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys	576
180 185 190	
AAT GCT GGT AAT GTG GGT GGT GAA GCA GGT GAT GCT GGG AAG GCT GCT Asn Ala Gly Asn Val Gly Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala	624
195 200 205	

GCT GCG GTT GCT GCT GTT AGT GGG GAG CAG ATA TTA AAA GCG ATT GTT Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val 210 215 220	672
CAT GCT GCT AAG GAT GGT GGT GAG AAG CAG GGT AAG AAG GCT GCG GAT His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp 225 230 235 240	720
CGT ACA AAT CCC ATT GAC GCG GCT ATT GGG GGT GCG GGT GAT AAT GAT Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp 245 250 255	768
GCT GCT GCG GCG TTT GCT ACT ATG AAG AAG GAT GAT CAG ATT GCT GCT Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala 260 265 270	816
GCT ATG GTT CTG AGG GGA ATG GCT AAG GAT GGG CAA TTT GCT TTG AAG Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys 275 280 285	864
GAT GCT GCT GCT GCT CAT GAA GGG ACT GTT AAG AAT GCT GTT GAT ATA Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile 290 295 300	912
ATA AAG GCT GCT GCG GAA GCT GCA AGT GCT GCA AGT GCT GCT ACT GGT Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly 305 310 315 320	960
AGT GCA GCA ATT GGG GAT GTT GTT AAT GGT AAT GGA GCA ACA GCA AAA Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys 325 330 335	1008
GGT GGT GAT GCG AAG AGT GTT AAT GGC ATT GCT AAG GGA Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly 340 345	1047

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 349 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Lys Asn Asn Asp His Asp Asn His Lys Gly Thr Val Lys Asn Ala Val 1 5 10 15
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Asp Met Ala Lys Ala Ala Glu Glu Ala Ala Ser Ala Ala Ser Ala Ala 20 25 30
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Thr Gly Asn Ala Ala Ile Gly Asp Val Val Lys Asn Ser Gly Ala Ala 35 40 45
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Ala Lys Gly Gly Glu Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile  
 50 55 60

Lys Gly Ile Val Asp Ala Ala Gly Lys Ala Asp Ala Lys Glu Gly Lys  
 65 70 75 80

Leu Asp Ala Thr Gly Ala Glu Gly Thr Thr Asn Val Asn Ala Gly Lys  
 85 90 95

Leu Phe Val Lys Arg Ala Ala Asp Asp Gly Gly Asp Ala Asp Asp Ala  
 100 105 110

Gly Lys Ala Ala Ala Val Ala Ala Ser Ala Ala Thr Gly Asn Ala  
 115 120 125

Ala Ile Gly Asp Val Val Asn Gly Asp Val Ala Lys Ala Lys Gly Gly  
 130 135 140

Asp Ala Ala Ser Val Asn Gly Ile Ala Lys Gly Ile Lys Gly Ile Val  
 145 150 155 160

Asp Ala Ala Glu Lys Ala Asp Ala Lys Glu Gly Lys Leu Asn Ala Ala  
 165 170 175

Gly Ala Glu Gly Thr Thr Asn Ala Asp Ala Gly Lys Leu Phe Val Lys  
 180 185 190

Asn Ala Gly Asn Val Gly Glu Ala Gly Asp Ala Gly Lys Ala Ala  
 195 200 205

Ala Ala Val Ala Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val  
 210 215 220

His Ala Ala Lys Asp Gly Gly Glu Lys Gln Gly Lys Lys Ala Ala Asp  
 225 230 235 240

Arg Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ala Gly Asp Asn Asp  
 245 250 255

Ala Ala Ala Ala Phe Ala Thr Met Lys Lys Asp Asp Gln Ile Ala Ala  
 260 265 270

Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu Lys  
 275 280 285

Asp Ala Ala Ala Ala His Glu Gly Thr Val Lys Asn Ala Val Asp Ile  
 290 295 300

Ile Lys Ala Ala Ala Glu Ala Ala Ser Ala Ala Ser Ala Ala Thr Gly  
 305 310 315 320

Ser Ala Ala Ile Gly Asp Val Val Asn Gly Asn Gly Ala Thr Ala Lys  
 325 330 335

Gly Gly Asp Ala Lys Ser Val Asn Gly Ile Ala Lys Gly  
 340 345

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCGCTGGAT GGTGGTGAGA AGCAGGGTAA GAAGGCTGCG GATCGTACAA ATCCCATTGA	60
CGCGGCTATT GGGGGTGCAG GTGATAATGA TGCTGCTGCG GCGTTTGCTA CTATGAAGAA	120
GGATGATCAG ATTGCTGCTG CTATGGTTCT GAGGGGAATG GCTAAGGATG GGCAATTGCG	180
TTTGAAGGAT GCTGCTGCTG CTCATGAAGG GACTGTTAAG AATGCTGTTG ATATAATAAA	240
GGCTGCTGCG GAAGCTGCAA GTGCTGCAAG TGCTGCTACT GGT	283

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTATTATAT CAACAGATTTC TTAACAGTCC CTTCATGAGC AGCAGCAGCA TCCTTCAAAG	60
CAAATTGCCCT ATCCTTAGCC ATTCCCCCTCA GAACCATAGC AGCAGCAATC TGATCATCCT	120
TCTTCATAGT AGCAAACGCC GCAGCAGCAT CATTATCACC CGCACCCCCA ATAGCCGCGT	180
CAATCGGATT TGTACGATCC GCAGCCTTCT TACCCCTGCTT CTCACCCACCA TCC	233

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGTGCAAGC TGGGTTGAAG AAGGTTGGGG ATGTTGTTAA GAATAGTGAG GCAAAAGATG	60
GTGATGCGGC GAGTGTAAAT GGGATTGCTA AGGGGATAAA GGGGATTGTT GATGCTGCTG	120
AGAAGGCTGA TGCAGAGGAA GGGAGTTGG TATGTGGCTG GTGCTGCTGG TGAAACTAAC	180
AAGGAAGCGG CCGC	194

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGCCGCTT GAGGAAGCTG CAAGTGCTGC AAGTGCTGCT ACTGGTAATG CAGCGATTGG	60
GGATGTTGTT AAGAATAGTG GGGCAGCAGC AAAAGGTGGT GAGGCAGCGA GTGTTAATGG	120
GATTGCTAAG GGGATAAAGG GGATTGTTGA TGCTGCTGGA AAGGCTGATG CGAAGGAAGG	180
GAAGTTGGAT GCTACTGGTG CTGAGGGTAC GACTAACGTG AATGCTGGGA AGTTGTTGT	240
GAAGAGGGCG GCTGATGATG GTGGTGTGATGC AGATGATGCT GGGAGGCTG CTGCTGCGGT	300
TGCTGCAAGT GCTGCTACTG GTAATGCAGC GATTGGAGAT GTTGTAAATG GTGATGTGGC	360
AAAACAAAAA	369

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGATGGTG ATGATAAGCA GGGTAAGAAG GCTGAGGATG CTACAAATCC GATTGACGCG	60
GCTATTGGGG GTGCAGGTGC GGGTGCTAAT GCTGCTGCGG CGTTAATAA TATGAAGAAG	120
GATGATCAGA TTGAGCGGCC GC	142

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGAAACTA ACAAGGATGC TGGGAAGTTG TTTGTGAAGA AGAATGGTGA TGATGGTGGT	60
GATGCGAGGTG ATGCTGGGAA GGCTGCTGCT GCGGTTGCTG CTGTTAGTGG GGAGCAGATA	120
TTAAAAGCGA TTGTTGATGC TGCTAAAGAT GGTGATAAGA CGGGGGTTAC TGATGTAAAG	180
GATGCTACAA ATCCGATTGA CGCGGCTATT	210

## (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATATAATAA AGGCTGCTGC GAAGCTGCAA GTGCTGCAAG TGCTGCTACT GGTAGTGCAG	60
CAATTGGGGA TGTGTGTTAAT GGTAATGGAG CAACAGCAAA AGGTGGTGAT GCGAAGTGTT	120
AATGGGATTG CTAAGGGGAT AAAGGGGATT GTTGATGCTG CTGAGAAGGC TGATGCGAAG	180
GAAGGGAAAGT TGGATGTGGC TGGTGATGCT GGTGAAACTA ACAAGGAAGC GGCGC	236

## (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAGAGGAT CTCATCACCA TCACCATCAC ACGGATCCCC CGGGCTGCAG GAATTCGCGG	60
CCGCTGAAGG CTGATGCGAA GGAAGGGAAG TTGGATGTGG CTGGTGCTGC TGGTGAAACT	120

AACAAGGATG CTGGGAAGTT GTTTGTGAAG AAGAATAATG AGGGTGGTGA AGCAAATGAT	180
GCTGGGAAGG CTGCTGCTG	199

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCGCTGGAT GATCAGATTG CTGCTGCTAT GGTTGTGAGG GGAATGGCTA AGGATGGGCA	60
GTTCGCTTTG AAGGATGATG CTGCTAAGGA TGGAGATAAA ACGGGGGTTG CTGCGGATGT	120
GAAAATCCGA TTGACGCGGC TATTGGGGGT GCGGATGCTG ATGCTGCGGC GTTTAATAAG	180
GAGGGGATGA AGAAGGATGA TCAGATTGCT GCTGCTATGG TTCTGAGGGG AATGGCTAAG	240
GATGGGCAGT TTGCTTTGAC GAATAATGCT GC	272

## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACTGTTAAGA ATGCTGTTGA TATAATAAAAG GCTGCTGCGG AAGCTGCAAG TGCTGCAAGT	60
GCTGCTACTG GTAGTGCAGC AATTGGGGAT GTTGTAAATG GTAATGGAGC AACAGCAAAA	120
GGTGGTGATG CGAAGAGTGT TAATGGGATT GCTAAGGGGA TAAAGGGGAT TGTTGATGCT	180
GCTGAGAAGG CTGATGCGAA GGAAGGGAAG TTGGATGTGG CTGGTGATGC TGGTGAAACT	240
AACAAGGATG CTGGGAAGTT GTTTGTGAAG AACAAATGGTA ATGAGGGTA	289

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

G CCG CTT ACA AAT CCG ATT GAC GCG GCT ATT GGG GGG AGT GCG GAT	46
Pro Leu Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ser Ala Asp	
1 5 10 15	
CGT AAT GCT GAG GCG TTT GAT AAG ATG AAG AAG GAT GAT CAG ATT GCT	94
Arg Asn Ala Glu Ala Phe Asp Lys Met Lys Lys Asp Asp Gln Ile Ala	
20 25 30	
GCT GCT ATG GTT CTG AGG GGA ATG GCT AAG GAT GGG CAG TTT GCT TTG	142
Ala Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu	
35 40 45	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Leu Thr Asn Pro Ile Asp Ala Ala Ile Gly Gly Ser Ala Asp Arg	
1 5 10 15	
Asn Ala Glu Ala Phe Asp Lys Met Lys Lys Asp Asp Gln Ile Ala Ala	
20 25 30	
Ala Met Val Leu Arg Gly Met Ala Lys Asp Gly Gln Phe Ala Leu	
35 40 45	